

GenBank Reference

Art. Part of 099585

Project

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DM nucleic - nucleic search, using sw model

Run on: April 6, 2004, 15:41:39 ; Search time: 1892 Seconds

(without alignments)

4.134 Million cell updates/sec

Title: perfect score: us-09-995-898a-1

Sequence: 1 atggcgccggccgagcgctg.....ggcattacatggccaggta 1476

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 0.0

Searched: 18 seqs, 2649592 residues

Total number of hits satisfying chosen parameters: 36

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database :

txt:

1: /home/sdavid/sdavid-tmp/apr04/kaufmann898/8388586.txt:*

2: /home/sdavid/sdavid-tmp/apr04/kaufmann898/8429214.txt:*

3: /home/sdavid/sdavid-tmp/apr04/kaufmann898/8518138.txt:*

4: /home/sdavid/sdavid-tmp/apr04/kaufmann898/9214222.txt:*

5: /home/sdavid/sdavid-tmp/apr04/kaufmann898/9797853.txt:*

6: /home/sdavid/sdavid-tmp/apr04/kaufmann898/11071629.txt:*

7: /home/sdavid/sdavid-tmp/apr04/kaufmann898/11071630.txt:*

8: /home/sdavid/sdavid-tmp/apr04/kaufmann898/11071631.txt:*

9: /home/sdavid/sdavid-tmp/apr04/kaufmann898/11071632.txt:*

10: /home/sdavid/sdavid-tmp/apr04/kaufmann898/11071692.txt:*

11: /home/sdavid/sdavid-tmp/apr04/kaufmann898/13162004.txt:*

12: /home/sdavid/sdavid-tmp/apr04/kaufmann898/1323743.txt:*

13: /home/sdavid/sdavid-tmp/apr04/kaufmann898/13442403.txt:*

14: /home/sdavid/sdavid-tmp/apr04/kaufmann898/13990004.txt:*

15: /home/sdavid/sdavid-tmp/apr04/kaufmann898/1572770.txt:*

16: /home/sdavid/sdavid-tmp/apr04/kaufmann898/1615113.txt:*

17: /home/sdavid/sdavid-tmp/apr04/kaufmann898/1644698.txt:*

18: /home/sdavid/sdavid-tmp/apr04/kaufmann898/1644698a.txt:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1

AL358412/C

LOCUS AL358412 172822 bp DNA lineal RTG 29-OCT-2000

DEFINITION Homo sapiens chromosome 1 clone RP11-509F14, *** SEQUENCING IN

ACCESSION AL358412

VERSION AL358412.8 GI:11071629

KEYWORDS HRC: HRCs PHASE1

SOURCE

ORGANISM Homo sapiens (human)

REFERENCE

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominoidea; Homo. (bases 1 to 172822)

AUTHORS Sims, S.

TITLE Direct Submission

JOURNAL Submitted (28-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire, Q310 USA, UK. E-mail: enquiries: humquery@sanger.ac.uk

COMMENT requests: clonerequest@sanger.ac.uk

[WARNING] On Nov 1, 2000 this sequence was replaced by a newer version gi:11071692. On Nov 1, 2000 this sequence version replaced gi:11043617.

----- Genome Center

Center: Sanger Centre

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: humquery@sanger.ac.uk

Project Information

Center project name: b509F14

----- Summary Statistics

Assembly program: XGAP4; version 4.5

Sequencing vector: plasmid; L08152; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Consensus quality: 166341 bases at least Q40

Consensus quality: 168310 bases at least Q30

Insert size: 171322; sum-of-contigs at least Q20

Insert size: 189168; agarose-fp

Quality coverage: 5.07x in Q20 bases; sum-of-contigs Quality coverage: 4.73x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently

* consists of 16 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will

QY	55	-	54	Db	32605	TCTTGAAACCCCTGGCACCGTGGTCAACAGATCTTGTGACTCGTGTCAATA	32546
Db	33685	AAAGCCTATATTATTGAGCACTTCTGAGCCAGCACCGATATTCTGGAGCT	33626	QY	55	-	54
QY	55	-	54	Db	32545	GATGGAATGTTGAACTCTAAGCTCATAGACCCATGAGAACCTAGAGAACAGTA	32486
Db	33625	CAAGACCCAGCCATCTCGAGATATTATTACTTTCTGGAAACTGAGAACAG	33566	QY	55	-	54
QY	55	-	54	Db	32485	CAGTCAGACTCGACTTGGAGTTGGCTGAGCTGAACTGATCTGATCTCACACT	32426
Db	33565	GTCTAGAGCAATTAGGSSATTCCTCAGAGAGATGGAGGAGCACAGAGAG	33506	QY	55	-	54
QY	55	-	54	Db	33505	AAGAGAGGGCTAAAGCAGCCGGCTAGTTGCTCCAGGGAGGACAGAGACAG	33446
Db	33445	GCTGTCCATTCCTGACTAGGCCAGCCAGGATGCTCCAGCCCGAGTGCCACAG	33386	QY	55	-	54
QY	55	-	54	Db	32425	AATAGCTGAGAGGCTTGTGTTCCACTCTGTAAACGGTTATAATTATAATGAAATA	32366
Db	33385	CGCGGTCTCTCTGGCTGATGAGGGAGCGTGTACCTGTTGGAGGGAGGGTGGCT	33326	QY	55	-	54
QY	55	-	54	Db	32365	CTACCTCCCTAGGGATGTTAGGATAAAGAGAAATGAGTGGAGTAACCTGTTAGACA	32306
Db	33325	TCTGTTCCCTTCACTGTCAAACCGAGACCTCTGTACCTGAAAGTATTAA	33266	QY	55	-	54
QY	55	-	54	Db	32305	GAACCTG3CTCACAGAACACAATAACATAGCTGCTATTATTTATTTATTTAT	32246
Db	33265	ATATACACAACTAACTATGGTGATGATTAGGAGTAAGTACGCCAGATCTAAGT	33206	QY	55	-	54
QY	55	-	54	Db	32245	TATTTATTTGAGACAGAGCTCACTCTGTACCCAGGCTGGAGTGGCAACT	32186
Db	33205	CAAACTCTGGCTCCACACAACTGACTGIGTAGCTCAGCCAACTTGTGTCACCTGATCTGT	33146	QY	55	-	54
QY	55	-	54	Db	32185	CGCTCACTGCAACCTCCACCTATGGGTCAAGCAATTCTGTCAGCTCCAAAG	32126
Db	33145	CTCTGAGCTTAGGCCCTTCATGGAAAGCAGCAATGACACCTACCCATAGGTGG	33086	QY	55	-	54
QY	55	-	54	Db	32125	TAGTGAGATGACAGGGCTGTGCCACCATGCCAACTTAATTGTGTTAGAAGAGA	32066
Db	33085	TCTGTCCTAACGGGTATGAGGTTAACATGTAAGAGCAAACTAGTGCTTCTGAC	33026	QY	55	-	54
QY	55	-	54	Db	32005	CCCTCTGCCCTCAAATGCTGGATCACAGGGTGGTTACATGCCGCTTACTGTC	31946
Db	33025	TGAAAGGCTCTAGAGGAATGGTGTAACTGTGTTTCTCATGTGACTAGCTCG	32966	QY	55	-	54
QY	55	-	54	Db	31945	TATTTATCATCATCGTTATCATCATCATGACACCTCGTAGATATGTCAGGAGAT	31886
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QY	55	-	54	Db	31885	CCCTGGAGGAAGTGCACATTGATCAAGTATTCAAGACTAGATGTTGAAACCCAGCA	31826
Db	32965	AACTCTGGGACTGTCTGCCATAGATACTTACAGTGCTTCAGACAGCTGGCT	32906	QY	55	-	54
QY	55	-	54	Db	31825	GTAAAGACACTGGTTAAACATCCAGAAATGCACTGGCTTGGACATGAGC	31766
Db	32845	GTGATACTGCCAGTAGAGAACAGGATGGTGGAGACGACCCACTTTGGT	32786	QY	55	-	54
QY	55	-	54	Db	31765	AGGAAGATGCTGATGAGCTCTGAGGTAGCTGTTGGAGAGAGCAGAACCGCT	31705
Db	32725	CCTCTGTCATTCACCGTATGGTTCATGACGGACTCTCA	32786	QY	55	-	54
QY	55	-	54	Db	31705	GGCAGGCCAGGCCAGCCAGCTCAGCAAGGCTCACAAACCTCTAAACAAATGTGAA	31646
Db	32785	CTAGAAGGTGATGGTAGGCCAGGGCTGGACAGCCATCCACAGACTGAGACCTC	32726	QY	55	-	54
QY	55	-	54	Db	31645	CTTATTCAGGCGCAAGGAAGGGATGAAACTGGGACTGGCTTATGATCGGTAT	31586
Db	32665	GGACCTGAAATTCTCCATGGGACCATGAGCTCTAGGGCAAGGAATGAGTGTCT	32606	QY	55	-	54
QY	55	-	54	Db	31585	TTCAGAAGATTAACAGTGTGAGAGAAAATGTCACAGAGGGAAATAGGGCTA	31526

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Db	31405	GAGGGAGACGGTGTGCAAGGCCGGAGTTGGAGTGTGGCTGGGGTGTCAAGGAG	31346	QY	55	-	54
Db	31345	GCAAAAGTGTGTTGGATGAGATATGGAGCAAGGAGACTGGAGTGTGGCTGGGGTGTCAAGGAG	31286	QY	55	-	54
Db	31285	GTAGGGCTTGTGTTGATGTTAAGAACCTCTGGAGTTGACCAAGGGTGTCAAGGAG	31226	QY	55	-	54
Db	31225	CCTGTAATCCAGCACTTGTGAGGGCAAGGTGGGGATCACTGTGGCTGGAGTCG	31166	QY	55	-	54
Db	31165	AGACCAAGCTTAGCCAAACATGGAAACCTCTCACTAAATAACCAAAATAACAG	31106	QY	55	-	54
Db	31105	GTTGTTGTTGCAACAAACTCTATCCAGCTACTGTGGCTAGGAGTGTCAAGGAGTGTCTGG	31046	QY	55	-	54
Db	31045	GAACCCGGAAGTGTGGAGGTGTGAGTGTGCACTGTACTCCGGCTGGAGTGTCTGG	30986	QY	55	-	54
Db	30985	GCGACGATAGACTCTGCCTCAAAATAATAATAAGACTTTGGTTCC	30926	QY	55	-	54
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Db	30865	TTTACATCCTCCTGAAAGATGGACTGTGAGGCAAGGTGTGTATTTGCT	30806	QY	55	-	54
Db	30805	GTTTGTAGAGACAGGGCTTGTGCTGGCCAGACTGAAAGTGCACTGGCAATCAG	30746	QY	55	-	54
Db	30745	GCAGCCTTGAACTCTGGGCTCAGGGAAACTCCACCTCACCTCTTACTCTCACC	30686	QY	55	-	54
Db	30685	TGTGCCCTGCTAAATTAAATAATTATTGTAGAGTGTGTCACTATGTG	30626	QY	55	-	54
Db	30625	TAGGCAAGGTAAATTCTGCTCAATGTTCTCTGGCTCGATGTCCAAAGTGCT	30566	QY	55	-	54
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Db	30505	CCTTTAATGATGTAGGTGTTCGGTTCTACCTAAAGCTCTGTAAATCAA	30446	QY	55	-	54
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QY	55	-----	QY	55	-----	Db	28165	GGCACAGGGCTGAGTACAGCCAGTCAGTGGTCCCTGAGTCAGTGAGCAC	28106
Db	29245	GCTGAGATTAACAGCCCTGCCCATACTCTCTCTAAATTTCATTTAGTAGAGCG	29186						
QY	55	-----	QY	55	-----	Db	28105	CTGCTGCGCTTGTGCTGCCAACTCAGTGGTCAAGACCCAGGAG	28046
Db	29185	AGTTTACCAAGTTGCCAAGACTGCTCTGAAATTCGACTCAGGATCTGCCAC	29126						
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Db	29125	CTTGACTCCAAAGTGTGGGATTAAGGCTAGGCTGAGCCACTGCGCCGCCATGAATA	29066						
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Db	29065	CTTCTTACCTGGGGACAGCCTTATAGCCTAGCTGTAACTGCGCCATGGGGTCTC	29006						
QY	55	-----	QY	146	ACCCAGGATGACCTATTGTTGCTGACTCTGCTGATCCATGCACTTAT	180			
Db	29005	ACACTTGTAACTGCGAGAGTCCCTGACTCTGCTGATCCATGCACTTAT	28946						
QY	55	-----	QY	181	-----	Db	27865	TGATGGAGACTGAGGGGGGGGGTGGGGCTGGAGGGCTCTCTGGACAGCTCAC	27806
Db	28945	GCCTGTCGACCATGTTCTGGGGCTGGAGCCAGACTGTTCCAGAACCCAGGAA	28886						
QY	55	-----	QY	181	-----	Db	27805	CCAGTGTGGCACACTGGCTACTCTGGGCCACTGGAGATGGATGCGCCGCA	27746
Db	28885	AACCAGGCCTGGCTGGCTGGTCTGAGATGGTCAAATTCACTACACCC	28826						
QY	55	-----	QY	181	-----	Db	27745	TTTGGAGAGGGTTTGTATAAGGCTCTGGAGGGAAAGTTGATGAGAGCAGT	27686
Db	28825	TCAATGCAAAACAGTCAAAAGGCTTATTACCTACAGATCTGAGGGAAAGTC	28766						
QY	55	-----	QY	181	-----	Db	27685	GTACAGGTGACCACTGCGGGGGGGTAACTTGTGAGGAAGTTGGTGTGGCA	27626
Db	28765	GAGTAGGGGGTCATCTCCATCTGGCTACATAGAAGCGGAATGAGTCAGGAA	28706						
QY	55	-----	QY	181	-----	Db	27565	GCCTCCAGCTGATCTGGCAACTAGGTACACAGCAGAGCTGTACTGGCA	27506
Db	28705	AAAGAAAGTGAAGCTGTGGCAATGAGTATATGTAAGGACTAGGGTGGGT	28646						
QY	55	-----	QY	181	-----	Db	27625	TGGATGTAAGCTGGGGCCAGGGATGAAATTCTCAAGTGGATGAGGGCTTGA	27566
Db	28645	CAGTTAAGTTGAGGCAATGCTGAATGATCCCTTAAGGATGAGGGTGGGAGTGG	28596						
QY	55	-----	QY	181	-----	Db	27505	ATTAGGATCCCTCAATGATCAGTCACTTTTCTTTTTTTGAGACAGAG	27446
Db	28585	GGAGCCCAGTTGCCGGAGGAGATGCCCTCGAAGTCTTATCTCTGGCACTGGCT	28526						
QY	55	-----	QY	181	-----	Db	27445	TCTTGTGTCACCAAGCTGGAGTCACTGCTGCTACTGCACTTCA	27386
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Db	28345	GGCATGGCAGGAGGCTGGGGATGTGGCTGAGAACAGAACAGGGCTGGCTTCA	28286						
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Db	28285	TATCTCAAGGATGCTCCCTCTGGGGCATTTGGTCTGTCAGTGTCTGCTG	28226						
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Db	24925	TGTTTCTGGGGTGTCTGTGAGGGTGTGCCAGAGACTACATTGAGTCAGTGGAC	24866	QY	181	-	180
QY	181	-	180	Db	23785	GCTTGGCGTCTGATTAAATCCAAATTCTTAAACACACATTATGAGTTAAATG	23726
Db	24865	TGGGAAATGGAAAGACTCGTCTCACTCAGTGGGGCACACCAACTGCGTCAGG	24806	QY	181	-	180
QY	181	-	180	Db	23725	TATATAGATAAACTGTCGCCATTAAAGTATACAAATTGATGAGTTTGACAAAGTG	23666
Db	24805	CTGGCTGGAAAGCAGGTGCGAGATGGTGGATAGCTTCACTTGTGGCTGGCTCCAGCTC	24746	QY	181	-	180
QY	181	-	180	Db	23665	GGCACCCAGTACCCACCCACAAATCAGAGTAAAGGTCTCTATCACCCAGAAAG	23606
Db	24745	CTTCTTCTCCCGTGGGATGCTTCCTCTCTCCCTGACATCACCTCC	24686	QY	181	-	180
QY	181	-	180	Db	23605	TTCCCTCATCCACTTGCATCAGGCCACAGATCTAGGAAACACAGACCTCTCGGAT	23546
Db	24685	GGGTTTTTGGCCTTAGACTCTTGGACTTAAGTTAGTGTGGTGTGGGGCTCTCGGAT	24626	QY	181	-	180
QY	181	-	180	Db	23545	ACACTGGTAACTTGGCTGTCAGCTCCCTGGTTGAGGTTTCAGATTC	24566
Db	24625	CTTGGTGCACAGACTGAAGCTGCACTTCAGCTCCCTGGTTGAGGTTTCAGATTC	24566	QY	181	-	180
QY	181	-	180	Db	23485	TACCTTGGTGTGGCTTCCCTGAGCTATGGGGCTATCGGGACTTC	24506
Db	24565	GGACTGAGTCATATGGCTCTTCTTCCACCTGCTGAGGCCATATGGGGACTTC	24506	QY	181	-	180
QY	181	-	180	Db	23425	TTACATGTAACAGTAGTTATTCTTTTATGCTGAGTAGTATGCCATGTATGACTA	23366
Db	24505	GCTTGTGATCCTGGAGCCAAATTCTCTTAATAAACTCCCTTCATATAAGTATAAC	24446	QY	181	-	180
QY	181	-	180	Db	23365	TGTATGACATTGTTAATCCATTTCCCGTCAGTGGATATTGGGTTCCAGTCTG	23306
Db	24445	CTATAGTCTGTTCTGGAGAACCTGACTAATAAAGGGTGTCTTCTTAA	23386	QY	181	-	180
QY	181	-	180	Db	23305	GGCAGGTTACATTGCTAGGGTGCATATGTTGCCCTCTGGCCCTCCAAATTGTC	23246
Db	24385	AACTCTAACTTATTGACTCTGTTGCTATGTTGATTTGAGTGTATT	24326	QY	181	-	180
QY	181	-	180	Db	23245	TCCCTGATGCAAATACATTACCCCTCCAAAGCCCCAAACCTCTCTTTT	23186
Db	24325	TCTGGCACTCAATATCTCACTTAAATACATGGTCCAGGCATTATTAGGAAGT	24266	QY	181	-	180
QY	181	-	180	Db	23185	TTTTTTGAAACAGAGTTGCTCTGTGCCCCAAGCTGGAGTGCAATGGTGATCT	23126
Db	24265	TTCTTAAATTATAGTTAGTATTGCTCTCTGTTGTTGATTCTCTCTTAGG	24206	QY	181	-	180
QY	181	-	180	Db	23125	CGCTCACTGCAACTCTGCCCTCCCGGGTCAGAGATTCTCTGCTGCCTCTGAG	23056
Db	24205	GAATCATATCACTGTTAGTGTGATCTCTTCTGTTGAGTGTCTTGGG	24146	QY	181	-	180
QY	181	-	180	Db	23065	TAGCTGGATTACAGGCATGCCACAGCTGGCTAAATTATATTAGTAGAA	23005
Db	24145	ACAGAGACTCACCTATAATCCAAGACTTGTGAGGCAATAGTAGGAGATGCTGA	24086	QY	181	-	180
QY	181	-	180	Db	23005	ATGGGGTTTACCGTGTAGCAGGCTGCTGACTCTGACCTCTGCTAGGCC	22945
Db	24085	GCCCAAGAGTTGAGACCAGCCTGGCAACATGGTGAAGGCCCTGCTCAATTAGAA	24026	QY	181	-	180
QY	181	-	180	Db	22885	AAACTCTAACCCATTTCAGCATCTACTCTAAGTCCAAGCTCTCATATCAGGATG	22826
Db	23965	TCTGCTCTAAATGAATAGTTCACTCTGAGTTAAACACTGATGCTCCAT	23906	QY	181	-	180
QY	181	-	180	Db	22825	GTTGACTGGAGGTGTTACTCTGAGGCCAAATTCTCTCCACTTATGAAACCTG	22766
Db	23905	GTGTGAGATTATCACACCTTATTTGTAATCTTCTCTGGTTACATTATTCTG	23846	QY	181	-	180

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Qy	181	-	Db	22705	CCCATTCAGAGAAATAGGAAGAGAAGAGTGAAGGTCCAAAGCAAGTCTA	22646	Qy	181	-	Db	21565	GCTAGGCTCCATACAAAGTACAGGACAGACTGGTAACACAGAATTATTTCTCA	21506
Qy	181	-	Db	22645	AAACCTCGAGGGCAAATTCCATTAGATTAAAGTCAAGATAAGCCTTGTGGCTCA	22586	Qy	181	-	Db	21505	AAATTCGAGGTTGAAAGTCCAAGGTCAAGGGTTGCTAGTTAGTTCTCTGAAGC	21446
Qy	181	-	Db	22585	GTGCTCTGCCCTTGGGCCCACTGGGGCGCACCCATCCCTTGGCTGGTGTGA	22526	Qy	181	-	Db	21445	CTCTCCTCTTGCTAGCACATGGCTGCTCTTGCTGTGCTGCTCCCT	21386
Qy	181	-	Db	22525	CCCTAACCTCGAGTCACTGTAGCAGGAGCTAGCCCTGCTGAACTAAGGGGACAG	22466	Qy	181	-	Db	21385	GTGCTGTTACTGGTAACTCTCTCCCTACAGTACACAGCTACTGGTAA	21326
Qy	181	-	Db	22405	GAATTTTCCATACTGTAGAGGATATTGCTGTTCAAGGAAATAGCTCOAGCTT	22345	Qy	181	-	Db	21323	GGGCCAGCTTATTACTCTTACCAATTACCTTAACTCTTAAGCTTAACTCTCAA	21266
Qy	181	-	Db	22345	GTCCCTTCTTGTAGATCCAGAAGTCCACAGCCTCCTTATTCTGCCATCTGT	22286	Qy	181	-	Db	21205	CATAATAGGCTTATGATTAAGCTGCTGTGACATTCATGACAGTCTTGTGTTA	21146
Qy	181	-	Db	22225	CTGCTTAATGGCTGATTAAGCTATGAGTCACCTCTGATCTTATGAAAGGTG	22166	Qy	181	-	Db	21208	ACCCATCTTACAAANITTCAAANTAGCCAGGATGGGGTACACCTGTAGCC	21026
Qy	181	-	Db	22165	TCTCTAGGCCACAACCTAGTGTCTCCAGAACATGCTTCATTTTTGCAAT	22106	Qy	181	-	Db	21145	ATATGTTCTATTCTCTAGATAAGATCTAGGAGTACAGCTGAGCTAGTGAG	21086
Qy	181	-	Db	22105	GTGGATAGGCTGAAATTCCAGCTCAAGTCTAGTCCTTGTACCTACATTC	22046	Qy	181	-	Db	21025	CTGCATCTCAGGGCTAGGGGGATCCCTGAGCCAGGGTTTAACTGAG	20966
Qy	181	-	Db	22045	TTTCATATCTCTCACATTACTATAAGCTAGAAAGAACCGGTGTAC	21986	Qy	181	-	Db	21085	ACCCATCTTACAAANITTCAAANTAGCCAGGATGGGGTACACCTGTAGCC	21026
Qy	181	-	Db	21985	CTTCAGCACTTGTAGAAATCTCTCTGCAAGCATCCAGTTATGCTTTAATT	21926	Qy	181	-	Db	20965	TGAATATGTTGACCACTGACCCAGGCCCTGGTGAAGAGTGTAGACTCTA	20906
Qy	181	-	Db	21925	ACTCTTGTATTATTATATCATTTGTAGATGCTGACTTAA	2166	Qy	181	-	Db	20905	AAAAAGAGAGAGGGGAGAAAGAAGAGAGAGGGGGAGGAGGGAGG	20846
Qy	181	-	Db	21805	AGATCACCTTCTCCAGTTCAATACACATCCTTCCACCTCACC	21746	Qy	181	-	Db	20785	CTATPACACGGAACCTGTGAGCTTCCAAAGTGTACTGTACCTGTGCT	20726
Qy	181	-	Db	21865	CTCTCTAATTCTGCAAAACACTAGAAGACACANTCAACAGTTCTGCACTTAAACA	21806	Qy	181	-	Db	20665	TTCATTTCACCATCTAGGAGTATGTAGTATTATAGGCTTAACTAAC	20606
Qy	181	-	Db	21715	AGATCACCTTGTATGCTATTCACCATAGCTTGTAGGAAATAGGTT	21686	Qy	181	-	Db	20605	TCCCTAATGATGATGTTGACATCTTCATGTCCTTATGGCCATTACATATCT	20546

Qy	181 -	180	Db	19465 ATTACTAGCTCTTACCTTTCATTGTTATGTTGATCATTCACTTCAGCT 19406
Db	20545 TTGTGAAGTGTACTTCAATTTCACCTTTTATTGGCTATTTCATT 20486		Qy	181 -
Qy	181 -	180	Db	19405 ATTATTATTCCATTATATTCTCATCTATGGTTAAATATTAAAG 19346
Db	20485 ATTAGTTATCTATGAAATCAACCTTATCAGTATGTTGATTTCCCCA 20426		Qy	181 -
Qy	181 -	180	Db	19345 GCGAGGTGGTGAATCACATCTGATACAGACTTAAAGGAGCTGAGGTGGAGGAT 19286
Db	20425 GTGGCTGGCCTTICATTGTTAGCTTTGGGGTTTTTTGGAA 20366		Qy	181 -
Qy	181 -	180	Db	19285 TGTGAGGCCAGAAGTTGAGACCGGCTAGGRACAAAGTGAGACCCCTCTACAG 19226
Db	20365 GAGAAATTTTAAATTGATAAAATCCAGTATATGGTTATAGACTATAC 20306		Qy	181 -
Qy	181 -	180	Db	19225 AATATTTTAAATTAGCTGGGCGAGAGTGGGGCATCCAGCCTGATAAC 19166
Db	20305 TCTACCCCACAAATCATATGTAAGGCCCTAACCTAAGGACTATTTGGAGATGAGC 20246		Qy	181 -
Qy	181 -	180	Db	19165 AGCACTTGGAGGCCAAGSCAGATGATCACCTGAGGTTGAGCACGC 19106
Db	20245 CTTAAGGAGGTTAATAGTAATGAGATCATAGGTGAGCCCTATCATAGAC 20186		Qy	181 -
Qy	181 -	180	Db	19105 GGCACATGGTAAACCCATCTTACTAAATAAAATTAGCAAGGGTGGTGA 19046
Db	20185 TGGTGTCTTATAAGAGAGGAGACACAGAGCGATGCAACAGAACGGCCTG 20126		Qy	181 -
Qy	181 -	180	Db	19045 GRCGCTGTAATCCAGCTACTTGGGGAGGTGAGGAGAATCTTGAAACCAGGG 18986
Db	20125 TGGAGCACAGCAAGATGAGGCCATCTGCAAGGCCAAGGAGAGGCTCAGTAGAAC 20066		Qy	181 -
Qy	181 -	180	Db	18985 AGGAGTTTCACTGAGGCCAGATGACACTGCACCCGGATGACAGGGAGA 18926
Db	20005 CTCGCTGTGGTCTTACCATGCGACCCCTACAGACTAATATCAGATTTCTC 19946		Qy	181 -
Qy	181 -	180	Db	18925 CTCTGCTAAAAAAAGAAGAAGAAATTAGCTGGGTAGGGTACTG 18866
Db	19945 TCAACAGTTAACGCTTGGCTCTAGCAATTGGCTCACCCAGGGCTAGANGAT 19886		Qy	181 -
Qy	181 -	180	Db	18865 TCCCACTGACTCAGAGACTAGGGAGGATCCTGGCCAGGAGTAGGGCTG 18806
Db	19885 TTCTCTCTATGTTCTCTGAAAGCTATATTAGCTTACATATTTCAC 19826		Qy	181 -
Qy	181 -	180	Db	18805 TGAGCTATTTGCCACTGCACTCCAGCTGCAACAGAGCAAGGGCTCAA 18746
Db	19825 TTCTCTCTCTGCTCTGTTAAAGCATCATCTATGGTTAATTGGCTT 19766		Qy	181 -
Qy	181 -	180	Db	18745 AAATATATTTTAAATTCAACTTCCCTTAGTCTCTTTGTTATTAACTTT 18686
Db	19765 GTATCCTCTGATTATCTCACTCTGAAATTGCTTTAAATATAT 19706		Qy	181 -
Qy	181 -	180	Db	18685 AACTGAATGTTTGCATAGAAGAAATCTTATGAGATACCTATTCTAAATTCT 18626
Db	19705 AATCTCTTCTGAGTTTCTAATGGTTTCTGCTCTG 19646		Qy	181 -
Qy	181 -	180	Db	18625 TAAGAATGTTGTTGTTAATTTGTTAATGGCTACAGCTGGTCAACCAATTGT 18566
Db	19645 ATCACTTTTACTGCTTTGCCATTGAGTATCAGGTTCCAGTTGATCTGTC 19586		Qy	181 -
Qy	181 -	180	Db	18505 TAGTATTATTTCTGCTCATCAATGCTCGGAGATTAATTCT 18446
Db	19585 TGGATATGTTGAGCATGTTCTGCTCTATCATTTATGCTAGCTATA 19526		Qy	181 -
Qy	181 -	180	Db	18445 TGTGAAAGGCGCTACTTCACTGTTGCTGTTGTTATAGAGGT 18386
Db	19525 ATTCATTTCTCTTATTCTATTAAGCTATGTTCTCTAAGT 19466		Qy	181 -

Db	18385	GAAGTGTGTTAGTAGGCACACATAGTTAGAATTTCCTGTCCTCTGGTGAATGGATC	18326	QY	181	-	180
Db	18325	ATTATCATATTATCTAATGTTCTTCATCTTGTAGTTAGTCTGGTGAATGGATC	1826	QY	181	-	180
Db	18265	TTTGTCTCTGTTAATAACTACACAGGGTCTTGTGTTAATTTGATAGATA	18206	QY	181	-	180
Db	18145	GTGAGCCCCATCTCAGCCTTCCATTCTACCTGGTCACTCCCAACCCAGGCAA	18086	QY	181	-	180
Db	18085	TCCTTGATCTCTTTCACATCCTACATCCAACTCCGTTAGCAAGTCTATTAGTC	18025	QY	181	-	180
Db	18025	TATTATTACCTCAAATAGATATTGAACTCCAGGCCCTTCCTACTCTCCACACATC	17966	QY	181	-	180
Db	17965	CTGTCACATCCTACATGGCCTCTGTGTTGACAGAGTATCTGTAACAAACA	17906	QY	181	-	180
Db	17905	TGTAGGCCAGGCACGGTGGCTCTGCTGTTAATCCCACACTTGGAGGCCAACGGG	17846	QY	181	-	180
Db	17845	TTGGTACCTGAGGTAGGAGTGGAGACCAACCTGGAGAACCTCTC	17786	QY	181	-	180
Db	17785	TACTAAANATAACAAATTAGCCAGGTGGTTACGGTGGCCGTATCCACATCTCG	17726	QY	181	-	180
Db	17725	GAGCTGAGGAGGAAATCACTGAAACCCAGGAGGGTGGAGCCAAAGATC	17666	QY	181	-	180
Db	17665	ATGCCACTGACCCACCTGGACAGAACAGACTCCATCAAATAATAATA	17606	QY	181	-	180
Db	17605	AAATAAAATGTTAGGTCTCCCTGGTCTCTGGTTACCCATTGTACTGCTTAACAAA	17546	QY	181	-	180
Db	17545	TACCTTAAAGTGTGTTAATTAATGTTGTTAATGCAATTAAATA	17486	QY	181	-	180
Db	17485	ATAGCAATTCTCTCCACACTTCTGAGCTGGAGTTAGGTCACAGGGCTC	17426	QY	181	-	180
Db	17365	GCATACGGAAAGGCACACTGTGTCCTCAAGTGGCCTCTCGTCGCTCTC	17306	QY	181	-	180
Db	17305	GCTCTCTGAACTTCAGGTTGGAGTCATGACCTGATGTCCTCTCACATCACAG	17246	QY	181	-	180
Db	17245	AGTACCTATCATGTCCTGGCATGCAGGGGCCATAACGCCCTGAATGACAAAC	17186	QY	181	-	180
Db	17185	ATATAGTATGTTGCTAGTACTAGAAATAGACGCCACGCAACTGCTGAGGGG	17126	QY	181	-	180
Db	17125	CATTACAGATGAGAAACTGAAATTAGGGAGGACCTGCCCCATGGTCCAAAGCTG	17066	QY	181	-	180
Db	17065	GGAGGGACAGGGCTGGGATTCACCTCCATCATCTGGTCCAGAACCTGAGCTCTGA	17006	QY	181	-	180
Db	17005	CAAGGCTGTTCTPATCCCTGTCAGCCAGTGCCTGCCCTGCTGACGGATGACCTAAAG	16946	QY	181	-	180
Db	16945	TTAGTCAGCCAAACAGGGAGCATACTGTTCTCAGTCTCAGTCCCTAACCGGAG	16886	QY	181	-	180
Db	16885	AGACTGAGTCTCTGGCCCAAGGCTCTCTCTCTCTCCCCAACGCTCTCCACCGTAGACG	16826	QY	181	-	180
Db	16825	CTGGCGGGAAGTGGAGAAGTGTGGGGGGACCAAGGACCTGCTGATGTTCTATAGTGCT	16766	QY	181	-	180
Db	16765	GAAGAACAGGACCTGACAAAGTCAAGTCAGGAGGAGGAGGAGGAGGAGGAGGAGG	16706	QY	181	-	180
Db	16705	CTAGTCCTCTGGTGAGTCCGAATCTGCTGTTGAGGTAGTCCTGTCAGTGTGCTGG	16646	QY	181	-	180
Db	16645	TTAGGACTGAGTGGAAAGCTCTCCATCGGGAGCTGTGCTAGTGTCTAGTGT	16586	QY	181	-	180
Db	16585	TCCTGTTCTCTGACCATCTGTCCTCCAAAGCAGGGAGGAGCTCCCTGGACCA	16526	QY	181	-	180
Db	16525	GCCTCTTGAGACGGGTGGAGGACCAAGCAGGGACCATGTCGGAGCC	16466	QY	181	-	180
Db	16465	AGGGAGTTAGGGAGCTCCAGCAGCAGCACTCAGGCACTCTGCTAAAT	16405	QY	181	-	180
Db	16405	GTCTTATTTCTGAGGACCATTTGTCATGACTACACAGGACTTATGTC	16346	QY	181	-	180
Db	16285	GGCCAGGGTGGGGTCACCCGTTGACCTGGAGGCCAAGCAGGTGA	16226	QY	181	-	180
Db	16225	TCACCTGAGGTTGGAGGTTGAGACCCCTGGCCACACATGAAACCAATCTG	16166	QY	181	-	180

QY	366 -	365	Db	15085 GTGCCCTGTAGTCCCAGCTCTGGGAGCTAAGGCAGGAGATGGCCGTGACCCAGGA 15026
Db	16165 AAAATAACAAATAATTAGCCAGCTGGTGGCAGCACCTGTAACTCCGAGCTACTCGGGAG 16106	365	QY	366 -
QY	366 -	365	Db	15025 GGCAGAGCTTCAGTGAGCTGAGATCGTCCACTGACTCAGCTGGTGACAGAGCA 14966
Db	16105 GCTGAGGCAGGAGAATCGCTTGAGCCAGGAGGGAGGTTCAGTGAGCCAGATCACG 16046	365	QY	366 -
QY	366 -	365	Db	14965 GACTCGCTCAAAATAATAATAATAATAAAAGGGCCAGCCATGGTGGCTACCA 14906
Db	16045 CCCGCACTCAGCTGGCGACAGGGCTCAAAAGAAATAATAACAAGA 15986	365	QY	366 -
QY	366 -	365	Db	14905 CCTGTAATCTGAGCACTTGGGAGCCGGCGATGGATCATTTGAGTCAGGAGTC 14846
Db	15985 AAAAAAACAAATTCTGTTGCAAAAGATTTCATAACTGAGAATTGTGGGG 15926	365	QY	366 -
QY	366 -	365	Db	14845 AGACCAAGCTGGCCACATGGTGAACCCCTGCTCTAAATAACAAAGTACCGCT 14786
Db	15925 TGGGGGGTTAAGATGATAGAAGAAAAATGTCCTAGCTTACTGGCAGAAATCAGTAT 15865	365	QY	366 -
QY	366 -	365	Db	14785 GTCTGTGSCACACACTGTTGCTTCAACTCAGAGACTCACAGAACTGTGATACGCT 15746
Db	15805 CTCTGAGGTTATTCCATCACACTGAGACTCACAGAACTGAGA 15806	365	QY	366 -
QY	366 -	365	Db	14725 GAACTTGGGAGGAGGTGAGTTGAGTCAGCTGAGCTGAGCACTCCAGCTGGT 14666
Db	15865 CTGACCTGGAGAGGGTTACAAAGGGGATAATGCCAGACAGTCCTCGTCTCGA 15626	365	QY	366 -
Db	15745 ATGATACCACTGACTGATACCGCTAGTAACCGGTGACATAGATGTGAACGGACTT 15686	365	QY	366 -
QY	366 -	365	Db	14605 GAATTGGCTCATGCACTCACAGCACACAAATGTCCCCAGCATGCACTGGTGA 14546
Db	15625 GAGCTGAGAGCTGTAACCTGCTGCCGGGCTCTCACAGTGTCAAGGAAATAAGGC 15566	365	QY	366 -
QY	366 -	365	Db	14495 AGTGTGTTACCCAGTCGGAGGCCACAGGCCACATCGAGGGCCTACTGATAA 14426
Db	15565 TTTAAGAGAGAGAGGAGACAGCTGATGCAAGGGAGAGATGAGAGAGCA 15506	365	QY	366 -
QY	366 -	365	Db	14425 GTCCAGAGCTCAATGGGGAGACAGGAACCTCAACGTCAGGACAGGAGTTG 14366
Db	15505 AGAAGAGATGATGTTGGAAGAGAGCTGCTCGTGGATGATAAGAGAGGA 15446	365	QY	366 -
QY	366 -	365	Db	14365 ATGTGCCAGCTAGGAAGAGAAATGTAATGTCATGCCATTCCCTCCATTTGTC 14306
Db	15445 CAGATGGTTAAGAGAAGGGGATGGAGGGATGAGGAGAACATGGAAATGG 15386	365	QY	366 -
QY	366 -	365	Db	14305 TTGGGCCGCTAGTGGTGGATGAGCCCTGCGCACACTGCTGGACACATCACC 14246
Db	15385 GAGGGAGGAGTTGGAGGATAGATGCCATTAGCAAAATAATGTTGGATAG 15326	365	QY	366 -
QY	366 -	365	Db	14245 AATCTGCGATTAATGTTAATCTCTCTGAGGAACTGCGCCCGAAT 14186
Db	15325 AGAGATGGGATAGGAGTTAGTCTCCAGAGAACATGACCAATAGA 15266	365	QY	366 -
QY	366 -	365	Db	14185 AATGTTTACGCTACTGGGTATCCTTACTGCGAGCTAAATGACACATAACTAAC 14126
Db	15265 TATATCAGATACTAAGAGGAGGCCAGCGGAGCGCTAGGAGTCAGACACATCTGCT 15206	365	QY	366 -
QY	366 -	365	Db	14125 CTCACAGGCCAGGACTGTGCTCACCTGTAATCCCATCTACTTGGAGGCCAGT 14066
Db	15205 GCACTTAGGAGGCCAGGGGGCGCTAGCGAGTCAGACACATCTGCT 15146	365	QY	366 -
QY	366 -	365	Db	14065 GGAAGATCTTGTAGGATGAGGAGCACATCAGTACAGCTAGGTTCAAGACCAGC 14006
QY	366 -	365	QY	366 -

Db	14005	CTAGGCAACTAGGGAGACCTCGTCTCACAAAAAAATTAATTGCTGGT	13946	Qy	366	-	
Qy	366	-		Db	12865	ACTTGAAAGGGGGTGTATTAGTTTCTCTGGCTGCCATATTCCCTGTCATGCCCTC	12806
Db	13945	ACGGTGGGGCACCTGTGGTCCAGCTATCTGGAGGCAAGTAGGAGATGTA	13886	Qy	366	-	
Qy	366	-		Db	12805	TCCATCTCAAGCCACTGGCAAGGCTAGAGGCCTCACAGACTATGGTAGGATG	12746
Db	13885	GCCCCAGGGCTCAAGCTGCACTGAGCATGTTCCATTAATTCCAGCTCGGTGA	13826	Qy	366	-	
Qy	366	-		Db	12745	GGAACTGAGACTCAGAGTGAGAAAGAACAGTAGATTAGAGAAAGCTAATTC	12686
Db	13825	CAGAGCAACACCCCTCTTAAGAAAGAAAATTAAACCATCACAGAGGAGAGAA	13766	Qy	366	-	
Qy	366	-		Db	12685	CCCTCCAGAAATACCTCATCTGAAAGCTGTTAGAGCAACTCAAG	12626
Db	13765	AGGAGATGGGTGATGAGATGGTGGTGGTATAGAGAAAGCAGCACATCCG	13706	Qy	366	-	
Qy	366	-		Db	12625	GCACGTCTCACAGGTAGAACCTGTTAGAGAAAGGAGAAACTGT	12566
Db	13705	GCAGGGAAAGGAGGCTGGAGGAGAGCAAGGAGGAGGAGGAGAACAGAA	13646	Qy	366	-	
Qy	366	-		Db	12565	CTGACTGCAAGAACTTCATCTGAAAGCTCATATGGCACAGAGCTG	12506
Db	13645	GGAAGGATCTGTAGAAAGGTGAGAGAAAGAGATGGATGATGGAAAGATGGATG	13586	Qy	366	-	
Qy	366	-		Db	12505	TAATGATGATTGATGATCTTATCCGAGAAAGGTGATGAGAAAGGAGAAATAGAA	13525
Db	13585	AGTGGTTAGAAGGCTACTGGCTAGATAAAAGGTGAGAGATAATGAAATAGAA	13526	Qy	366	-	
Qy	366	-		Db	12445	CCTGGTTCTCTGCCCTTATAGTAATGAGAGAGAGAGAGAAATGGAAAGGACCG	12446
Db	13525	AGGAGGATAGAAAGAAAATATTGGTTAGAAAGGATGATGAGAAAGGAGGTT	13466	Qy	366	-	
Qy	366	-		Db	12385	AACTTAAACAGAAGGAAAGGACTGTGATTGGGGTTCTCAACTATGCAAA	12326
Db	13465	GGGAAGGAGGAGGAGGATGGATGATGATGGATGAGAAAGGAGG	13406	Qy	366	-	
Qy	366	-		Db	12325	ACAATAAATTAAGAGATTGATGCTGGGACAGTGCTATGCCATACCCAGCACTT	12266
Db	13405	GATAAGAAGGAGAGGAGGAGGCTCTCGCTAGAGATGGAGAGAACACACATAT	13346	Qy	366	-	
Qy	366	-		Db	12265	TGAGACTCCGGCCAGAGCATCACCTGAGGTAGGAGGATCATCTGAAACCAAGGGAGG	12206
Db	13345	TGCTGAAATGGTAGGAATAAGACATTAGAGAAATAAGGAAGAACAAAGATTTAA	13286	Qy	366	-	
Qy	366	-		Db	12205	TTGGGAAACTCGCTCTACTAAATAACAAATTAGTGTTGGGGCGACCT	12146
Db	13285	ATGTTTCATTAATTGCTCTGAAATTCTCTGATTTCTGACCCCAT	13226	Qy	366	-	
Qy	366	-		Db	12145	GTAATCCCAGTACTCGAGGGCTGAGGTGGGGATCATCTGAAACCAAGGGAGG	12086
Db	13225	CCCAAGCCAGGGTATCCTCTGCTTACACTCCCTCAACTTTCTCTCUTCAT	13166	Qy	366	-	
Qy	366	-		Db	12085	TTCAGTGAGGCCAAGATCATGCCACTGCTGACTCCAGCTGGGGTGACAGCAAG	12026
Db	13165	TGAGCCGGTCACTTCTTGTGATTTACCTAACCTCAACTTTCAGC	13106	Qy	366	-	
Qy	366	-		Db	12025	CCATTCACAAAAAAAGAGATGCTCCAAAGTGACATAGAGAACAGC	11966
Db	13105	TCTGAAAGTCAGGATACAGGAGCTCATCCGATTCCTCACTCCCTCTGA	13046	Qy	366	-	
Qy	366	-		Db	11905	AAGCTCTTGAGAGATTTAGATATACTCACGTCCTCAATCACAGGGAC	11846
Db	12985	GAAGAAGGCCACATGTTACCTCACACACAGGCAAAAGTGAATGGTGTCA	12926	Qy	366	-	
Qy	366	-		Db	11845	TTCTAGGAAGCTGAGAGATGTCCTGAGCCATCTGAGCTGGAGCAAAAGTAGAGA	11786
Db	12925	AGATCCCTGCTGGCTGGGATCAGGAAGGCTGATGGCAATTAGTTAGTTAGA	12866				

Qy	366	-	365	Db	10705	TCGGTGGCACTAGGAATCTTAACTAACGTTATAGACTGTTATGGTTGAATGTCCTCT	10546
Db	11785	GGGCCTTATCAGAAAGGATCTGGGACTTATCTAAATGCACTGGATTC	11726	Qy	366	-	365
Qy	366	-	365	Db	10645	AAACTCTGTGACATTAACTATCATCTATGATGCCATTAGAAGTGCCCTGTAA	10586
Db	11725	CCCATGACATCCATAGGAGACCCCTAAAGTCTCTGAGAGCTTACATCCAGAAAC	11666	Qy	366	-	365
Qy	366	-	365	Db	10585	GGTGTATTAGCTTAAAGGCTGATAGGAGTAACTGAACTAAGGCTGTTGACTC	11526
Db	11665	GTTCCTTGTGATTAATGGACACAGAGAGTAACTGAACTAAGGCTGTTGACTC	11606	Qy	366	-	365
Qy	366	-	365	Db	10525	TGTGTTATCAGAATGGATGTTAAAGTGAGTCTGCTCCAGGGCAGTGGCTATGC	10466
Db	11605	CAAGTTCTACTGTGAGTGGTAAACTACTTAGCTGCAACACCTGCTACT	11546	Qy	366	-	365
Qy	366	-	365	Db	10465	CACTCAGCACTTTSGGGSCCAAGACTTGTGTTGAGACCGCTGCCCC	10406
Db	11545	TTAGTGAAMGGAAGGATATCTAGACGGTGAAACCGAGCTCAAGGGCAGTCAAG	11486	Qy	366	-	365
Qy	366	-	365	Db	10405	ATGGTGAAGCTGCTCTACTAAATAACAAAGTCTCCGGAGTGCTGGGGCC	10346
Db	11485	AGCGAAAGGAGATCTTCCAGGCTCTGAACTTAATGGAGTTCTGCGGATTC	11426	Qy	366	-	365
Qy	366	-	365	Db	10345	CTGTAATCCCAGCTCTCAGGAGGCCAACGAGGATGCGATGATCCGGAGGAGA	10286
Db	11425	AACTGCACTGGACCATGACCTGATGCCCCATGTCGACCCAGATG	11366	Qy	366	-	365
Qy	366	-	365	Db	10285	GGTGCAGTGAGCTGAGATGCCCGTCACTCCAGCTGGTGTAGACGAACTCT	10226
Db	11365	TCTGCAACTGTTATCTGCTGCTGCTCCACATTATGTCGAGAGAAACTTGT	11306	Qy	366	-	365
Qy	366	-	365	Db	10225	GTCTAAALAAALAAALAAAGAGGAACAAAGAAGAGAAGAGAAGAAAGAAGA	10166
Db	11305	TGTCGCCCCAACAGATAGAGAGAACTGTTACCCGAGAGTTACTGACTGACTAGCC	11246	Qy	366	-	365
Qy	366	-	365	Db	10165	AAGAAAGGAGGAAGGAAGGAAGGAAGGAGGAAGGAAGGAAGAAAGAAAGAA	10106
Db	11245	CAAGTCTTATTGACTCTGACTTAGATGTTGATGGGATTGAGTGTGATGCTGTA	11186	Qy	366	-	365
Qy	366	-	365	Db	10105	GAAGAAACAAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	10046
Db	11185	ATGAGATGAGACTTGGGGACATGGGATGGATGGATTGATGAAAGAGA	11126	Qy	366	-	365
Qy	366	-	365	Db	10045	AAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAG	9986
Db	11125	TGAGGTTGGATCCAGGCCAACACTGTAATCCAGACATTGGGGCCGGAGC	11066	Qy	366	-	365
Qy	366	-	365	Db	9985	AAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAG	9926
Db	11065	GTGAGATCACCTGAGGTCGGCACTTCGAGACCCGCTAACACCATGAGAACCCATCT	11006	Qy	366	-	365
Qy	366	-	365	Db	9925	NN	9866
Db	11005	CTRACTAAATAACAAATTAGCCAAAGCATGGTAGACATGCCATTATCCAGCTACTCG	10946	Qy	366	-	365
Qy	366	-	365	Db	9805	CCCTTCCACCTGCCACCATGGATGAAAGGAGAAAGGCCCTCACAGATGCCAGTGC	9746
Db	10945	GGAGGTGAGGAGTAGAATCCCTGAAACCCGGGGACAGAGCTGGTGTGAGCGAGAT	10886	Qy	366	-	365
Qy	366	-	365	Db	9745	TGCCTCTGAGCTTCAAGTCCAGAAACTGAGCCAAATGACTCTGTCATTATA	9686
Db	10885	CACGCCATTGCACTCCAGCTGGCACAGAGGTGAAACTCCATCTAAAGAAAGAA	10826	Qy	366	-	365
Qy	366	-	365	Db	9695	TTACCCAGCCCTGTGATATCTGTAATAACACACAAATAGTGTGAGATCTCA	9626
Db	10765	ATCCTCTAAAGGTGCTGCCCCATACTCCAGAACCTAGAAATAGTGTGAGCTAT	10706	Qy	366	-	365

Db	9625	AATACTGAGGTTATCCTGGATAATCCAGATGCCCCAATCTAATCCATGACCCCTTAA	9566	Qy	509	-	508
Qy	366	-	-	365	Db	8485	AGAAAACTGAAATACTAGATAAGCTCTAAGANGCAGCAGAAAGTACCCAGAGATGC
Db	9565	ACTTCTCCAGATGGAGGGAGAGAGAACTGGCAGAAGGGAGTCAGAGATTGAG	9506	Qy	509	-	508
Qy	366	-	-	365	Db	8425	CACACATCACTCTGGTATATCCATTAGATTTGTTCTGTATGATGAA
Db	9505	CATAAACAGGACTCATGGTCCGTTCTGGTTGACGATGAGTGGTAACCTGATGAA	9446	Qy	509	-	508
Qy	366	-	-	365	Db	8365	TAGTCGATTATTATG3CAAGGGTGCAGACTTCCCGAAGAAGGCCAGATAGTCG
Db	9445	ATATGGGGTGCCTTCGGAGCTGAGAGGGCTCCACTAACATCGCCAGGAACAGGC	9386	Qy	509	-	508
Qy	366	-	-	365	Db	8305	TATGTTTGGCTCATGGGGTATGTCCTCAGGACTACTAACGCTCAGTTATAGCA
Db	9385	CACACCCCTAACAGCACAAGAACTAAGTTTCTGAAACCCAAAGGGGCTTGGAGTG	9326	Qy	509	-	508
Qy	366	-	-	365	Db	8245	CAAAGGAGCGTACGCTATACTGAAATGCGCATGCTGGTCCAGTAAACTGT
Db	9265	TGGACTCTGACTAGAGAACTGTGAGATAATAAGTTGATCATTTAAGCACTGTG	9206	Qy	509	-	508
Qy	366	-	-	365	Db	8125	TGGAGGATTACCTAGCCAGGAGTCAGACAGCAGCTGGGACATGTGAACATTA
Db	9205	TGTGTTGTAATTGTTATGACGATAAGAATGATCCAGATGGGAGTCGAC	9146	Qy	509	-	508
Qy	366	-	-	365	Db	8065	TCCCTACAAAGAAAGAAAGCTGGGTGGTGTGATGCTTGTCAGCTGCTTG
Db	9145	GGCCAGTGACATGTGGAGGGCACCCAGGGGATGGATGGCATGAGAGAGGTCAGC	9086	Qy	509	-	508
Qy	366	-	-	365	Db	8005	GGATGTGAGGAGGATGCTGAGGCCAGGAGCAGGCACAGTGACCATGATC
Db	9085	ATATGAGCTGCCAGGTACCTCTCTCTAAGCTCAGTTTCTCTATGAAATGA	9026	Qy	509	-	508
Qy	366	-	-	365	Db	7945	GCACCACTTCACTTTAGTCGGGACACAGTGGAGACCTTGTCTAAAAAAACAAA
Db	9025	GGAGTAGTGATATCTCCCTCCAGGGTCACTGCAAGGTGAATAACAGATTTAAGTC	8966	Qy	509	-	508
Qy	366	-	-	365	Db	7885	TAAAACTTTTACATAAAAGTGCCACCACTGTCCTGGCCCTGGCTCTGTA
Db	8965	TAGTGTGACAAAGAAGTGTGAAACATGCTAGTGTCTTCATTCCAAGGAGCTC	8906	Qy	509	-	508
Qy	366	-	-	365	Db	7825	ATGTTCTTCCACTAAAGTACATTCACCTCCGATTTTGCACTCAGGGTCT
Db	8905	TGGTCTGGGGATGTGGGGTACTGAGGGTCACTGACAGTCCTGGCTGTGTT	8846	Qy	509	-	508
Qy	366	-	-	365	Db	7765	GGGGATAATAGATCGAAATCCAGGGTCTCTCCCTTAAGAACCTCAAAATATCTA
Db	8845	TCTGCAGTGGAGCCGCCAACCTGTCCTGGTCTCACCAAGGGAGATCTGAGT	8786	Qy	509	-	508
Qy	421	GGCAATGCGCAGTGTACCTGCCCCACTGTTCTGAAAGTGTAGGGT	480	Db	7705	GACCACTGCCATAAGAAATAATGCAAGCCACATGTGCAGTTAAGTGT	
Db	8785	GGCAATGCGCAGTGTACCTGCCCCCTGCACTGTTCTGAAAGTGTAGGGT	8726	Qy	509	-	508
Qy	481	GCATTTGGGGGGGGGGCCGACCA	-	Db	7645	CCATGTTAAATTGTAAGAGACAGGTTAACTGAGATTAAACGATTTACTTC	
Db	8725	GCATTTGGGGGGGGGGCCGACCAAGTGGAGTCCTCTGCCCCAGCTA	8666	Qy	509	-	508
Qy	509	-	-	508	Db	7585	ATCCATTGATGGTATCATGAGCAATTCTGATAGTGTGATTGAGATCTTACAT
Db	8665	GGCCCGCTCCTCCACCCCTCTACTCAGGTCTTCTCACCTCCAGCTCTGC	8606	Qy	509	-	508
Qy	509	-	-	508	Db	7525	TCTTTCTACTACGGCTTAACTGAGTGTGTTTGTACTTGAAACACTCTCAGT
Db	8605	CCCTCTCAGGAAGTCCTCTGACTCTGACTCTGAGCTGAGCCCTAA	8546	Qy	509	-	508
Qy	509	-	-	508	Db	7465	TGGACAGATGCAATTCACTCAGTGTACGGGGGGCCAGTCCATACACCA
Db	8545	ATCTGATCAAGATGATGACTACAGGAGGCTCTGCCAAGTCACAGTCAGTC	8486	-	-	-	-

QY	509	-----	Db	6325 GCTTCTCTGGCTGCCATCTCTCTCTGATAGTACTGCTGTTAGTAATGCGCAGGGGTG
Db	7405 CAGTCAGCATCTGTAGAGGTTCTCCACTCTGATAGACTAGAGACCCAAAGATGGA	7346	QY	742 ATCTGGAAGGCCCTCATGGGAAACCCCTGTTCAACGGGAAAGATGCCAGGGCCCT
QY	509	-----	Db	6265 ATCTGGAAGACCTCATGGGAAACCCCTGTTCAACGGGAAAGATGCCAGGGCCCT
Db	7345 AAGCTGAAAGAATCTGCTCTGAGTAGGGACCTTAATGGGGTGCACGGCAGGGGACC	7286	QY	801 ----- 800
QY	509	-----	Db	6205 GTATGAAATCTGGGGCTGAGCAGTGGGGTGGAGTAAGGGAGTGGC
Db	7285 CCAAGTGTAGGCTTGTGACCATGGCTATCCCACCTCTAGACTCAGCTGAAAGA	7226	QY	801 ----- 800
QY	509	-----	Db	6085 CTATCTGTGCTGAATTCCACCATAGTAATGCTTCAATTAGTCTGAAATAATG
Db	7225 ACTCAGTAGCTGGAAAGCTCTCTCAATGCTTAACCTTAATGCGAGGAAGATA	7166	QY	801 ----- 800
QY	509	-----	Db	6025 GCAACAGGCCCTGGAGGGAGCAGTGCCCTGGCTTGTAGATAATAACTCACCTC
Db	7105 ACAGAGAGACCTGCTATAAAALATAATTAAAAAAATACCCAGGTATGGTGGGT	7046	QY	801 ----- 800
QY	509	-----	Db	5965 TGCCTAAGGATGTGTAGCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGACA
Db	7045 GGATCTGTAGTCCCTAGTACTGAGAGCTGAGGGAGTGCCTTGAGCCAGGAG	6986	QY	801 ----- 800
QY	509	-----	Db	6025 GCAACAGGCCCTGGAGGGAGCAGTGCCCTGGCTTGTAGATAATAACTCACCTC
Db	6985 TTGAGGCTGAGTGTGATACACACTGACTTGGCTGGTGACAGAACAA	6926	QY	801 ----- 800
QY	509	-----	Db	5905 CTCAAAAGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGACA
Db	6925 ACCCTATCCCTACAAAAAAACTAALAAAAAAATAAACCCATTACAGTCT	6866	QY	801 ----- 800
QY	509	-----	Db	5845 TTACACTTAACTCAGGATAAGCTGTGTCTGGTACCTGGAGTGGTTCTCCCTGGTC
Db	6865 GCCAACCCCACTCTGCTGGCTGGTGAACCACTCCCCACAGAGCTGTGCCATCTC	6806	QY	801 ----- 800
QY	509	-----	Db	5785 TGTCTGGCTCTCCTCTAGAACCTAGGGGGAGCTGGGGAGGGAGGCCAAGGGTGA
Db	6805 TGCTTCTTTCACAAACAGACCCATTTCAGTCAGTCTCCCATGGCAGCAGCCAGATC	6746	QY	801 ----- 800
QY	553 ACTCTCCAGCAGCTCCAGCGAAACCACTGCTCAGTCCAGAACCTAACAGTC	612	Db	5725 TATAAGGTGGCCCTGTCAGATCAGGACTCTGGAGGGAGCTGGCATATGGAGGCTC
Db	6745 ACTCTCCACCCAGCTCCAGCGAACCCATGCTCCAGGGAGAACCTCTAACAGTC	6686	QY	801 ----- 800
QY	613 AGTGTCCGAAATAAGCAGTCTCTAACCCACCTGCTCTGGTGGAGGRCCT	668	Db	5605 AAAGGGACATTCCAAATTCTGGCTCCAGGAACTGTGGAGATACTCCACACTGTC
Db	6685 AGTGTCCGAAATAAGCAGCTCTAACCCACCTGCTCTGGAGGRCCT	6626	QY	801 ----- 800
QY	669 ----- /	668	Db	5545 AAGGTGACACCTGGGTAGAGAATGTCAGGAGGAGGAGGAGGAGGAGGAGGAGG
Db	6625 GGGTATCANGTGGTCAGAAGAGAACTTCCCTGGGACTCTGGACAC	6566	QY	801 ----- 800
QY	669 -----	668	Db	5485 AGAGCAACCCAGCTGGATTTCAGCTCCAGGGCTGACCCCAATGGCTTCTCTGGC
Db	6505 TGTCTTGGCCAGCTTACATAATGCCCAAACCTTGGTTGCACAGTCAGGATGGT	6446	QY	801 ----- 800
QY	669 -----	668	Db	5425 CTCTGGAGGCCACATGCCCTGCACTGCCAGGGCTGACGGCAACGGCT
Db	6445 TTATCTCTGGAGGATTAATAGGGCTCATGAGTGTGAAGCACTCGGCACAGGCTG	6386	QY	801 ----- 800
QY	669 ----- / AGAAGCACTGG	681	Db	5305 TCTGAGGTGGCTGCCAGTCAGCTCTGAGTGCAGGATTAAGTGCAGTAGCC
Db	6385 TAGACAGAGCCATTTGCTGCTGAGGATGCTGAGTGTGAGTGTGAGGCTG	6326	QY	801 ----- 800

VERSION	AL358412.9	GI:	11071692
KEYWORDS	HTG; HTGS; PHASEI.		
SOURCE	Homo sapiens (human)		
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 173352)		
AUTHORS	Sim, S.		
TITLE	Direct Submission		
JOURNAL	Submitted (29-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk. Clone requests: clonequery@sanger.ac.uk		
COMMENT	On Nov 1, 2000 this sequence version replaced gi:11071629. ----- Genome Center		
Center code:	SC		
Web site:	http://www.sanger.ac.uk		
Center:	Sanger Centre		
Center code:	SC		
Contact:	humquery@sanger.ac.uk		
----- Project Information			
Center project name:	ba509F14		
Assembly program:	XGAP4; version 4.5		
Sequencing vector:	Plasmid; Lu8752; 100% of reads		
Chemistry:	Dye-terminator Big Dye; 100% of reads		
Consensus Quality:	167382 bases at least Q40		
Consensus Quality:	169011 bases at least Q30		
Insert size:	170100 bases at least Q20		
Insert size:	118182; sum-of-contigs		
Quality coverage:	5.54x in Q20 bases; sum-of-contigs		
Coverage:	5.18x in Q20 bases; agarose-fp		

NOTE:	This is a 'working draft' sequence. It currently		
	consists of 16 contigs. The true order of the pieces		
	is not known and their order in this sequence record is		
	arbitrary. Gaps between the contigs are represented as		
	runs of N, but the exact sizes of the gaps are unknown.		
	This record will be updated with the finished sequence		
	as soon as it is available and the accession number will		
	be preserved.		
	1		
	9825: contig of 9825 bp in length		
	9826 9925: gap of 100 bp		
	9925 26225: contig of 16300 bp in length		
	26226 26325: gap of 100 bp		
	26326 29517: contig of 3192 bp in length		
	29518 29617: gap of 100 bp		
	29618 35632: contig of 6015 bp in length		
	35633 35732: gap of 100 bp		
	35733 49745: contig of 14013 bp in length		
	49746 49845: gap of 100 bp		
	49846 66204: contig of 16559 bp in length		
	66205 66304: gap of 100 bp		
	66305 66332: contig of 6535 bp in length		
	66332 72939: gap of 100 bp		
	72939 72840: contig of 10783 bp in length		
	72840 83722: contig of 711 bp in length		
	83723 83823: gap of 100 bp		
	83823 91894: contig of 8022 bp in length		
	91895 91994: gap of 100 bp		
	91995 103783: contig of 11789 bp in length		
	103784 103883: gap of 100 bp		
	103883 103894: contig of 711 bp in length		
	103894 11095: gap of 100 bp		
	11095 111094: gap of 100 bp		
	111095 127550: contig of 16456 bp in length		
	127551 127650: gap of 100 bp		
	127651 137959: contig of 10309 bp in length		
	137959 138059: gap of 100 bp		
	138059 138060: contig of 13437 bp in length		
	138060 151497: gap of 100 bp		
	151497 151596: gap of 100 bp		
	151597 154339: contig of 2943 bp in length		
	154339 154639: gap of 100 bp		
	154639 173352: contig of 18713 bp in length.		
FEATURES	Source		
	Location/Qualifiers		